

# Supplementary Table for: Measuring Microsatellite Conservation in Mammalian Evolution with a Phylogenetic Birth-Death Model

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This table contains the results of the linear analysis of the relationship between our conservation score, the logit of the probability of the low death rate, and four covariates: distance to transcription start site, motif, length and functional region. The results shown are all factors significantly associated with conservation after false discovery rate correction.

	sorted.qvalues	reg.coef
Intercept: function: 3' UTR	6.1E-143	1.7E+00
distance to promoter	3.8E-121	-1.6E-04
function: intergenic	6.2E-93	-1.3E+00
function: intron	5.7E-90	-1.2E+00
length	9.5E-82	1.8E-02
motif: AC	2.7E-42	4.7E-01
motif: AT	2.1E-38	-6.9E-01
motif: C	1.5E-31	-1.2E+00
motif: CCG	4.9E-25	4.7E-01
motif: AGC	5.3E-25	6.8E-01
motif: AGG	4.6E-20	4.7E-01
motif: AAT	1.9E-12	-3.9E-01
motif: AATG	6.5E-12	4.4E-01
motif: CCCCGG	1.9E-11	-1.7E+00
motif: ATACCT	6.7E-11	-1.3E+01
motif: CCCCG	1.8E-10	-6.0E-01
motif: AAC	7.3E-10	-3.9E-01
motif: CG	1.8E-07	8.7E-01
motif: AGCCCC	6.8E-07	-1.4E+00
function: coding	1.9E-06	3.8E-01
motif: CCCCCG	6.8E-06	-9.6E-01
motif: CCGCG	8.6E-06	-1.0E+00
motif: AGGGG	9.1E-06	-5.8E-01
motif: ACCCC	1.8E-05	-6.8E-01
motif: AAAAC	2.6E-05	-3.1E-01
motif: ATAG	6.7E-05	-5.6E-01
motif: AGGGC	1.3E-04	-7.7E-01
motif: ACACGC	1.8E-04	2.5E+00
motif: AGGC	2.0E-04	-3.7E-01
motif: CCGG	2.5E-04	-7.4E-01
motif: AGGGGC	2.7E-04	-1.4E+00
motif: ACCCCC	5.7E-04	-8.1E-01
motif: CCCG	8.2E-04	-2.6E-01
motif: CCCGCG	9.4E-04	-1.5E+00
motif: AAAAT	1.0E-03	-3.9E-01
function: 5UTR	1.3E-03	-2.6E-01
motif: ATAC	1.5E-03	-3.8E-01
motif: ACG	1.6E-03	1.2E+00
motif: AAAC	2.0E-03	-2.0E-01
motif: AGCGG	2.8E-03	-1.6E+00
motif: AGGCG	3.2E-03	-1.3E+00
motif: CCCGG	3.7E-03	-5.5E-01
motif: AGCCG	4.0E-03	-1.2E+00
motif: AAATT	5.0E-03	-7.1E-01
motif: ACAG	5.2E-03	3.4E-01
motif: ACCC	5.3E-03	-2.6E-01
motif: AATT	5.3E-03	-4.0E-01
motif: AAGCCG	6.0E-03	5.2E+00